SEQUENCE LISTING

<110> LUDWIG INSTITUTE FOR CANCER RESEARCH

<120> TUMOR ASSOCIATED ANTIGEN ENCODED BY THE REVERSE STRAND
      OF A NEW UBIQUITOUSLY EXPRESSED GENE

<130> L0461/7034WO

<150> US 60/085,318
<151> 1998-05-13

<160> 11

<170> FastSEQ for Window Version 3.0

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<220>
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<222> 738..989

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ttttctcctc tggtgacaat atagtgtcca acacttggaa gtgattttta agaatgttta     180
tttaaattaa aaggatggat ttccaaggaa aaaaaataag gaaaggaaa  gaaaaaactg     240
aacagaaaac gcaaaagtat cagtttggtc actaaccttt gcaaggatac cttttttattt    300
tctttaagat tcctgttgtt tatacacaga ttttaagttt actcctactg ctgacccaag     360
tgaaattcct tctccagtca cagtgtcaac ctctaccccc caactgcaac gagagttttg     420
aggggcatca atcacaccga gaagtcacag ccccctcaacc actgaggtgt ggggggggtag    480
ggatctgcat ttcttcatat caaccccaca ctatagggca cctaaatggg tgggcggtgg     540
gggagaccga ctcacttgag tttcttgaag gcttcctggc ctccagccac gtaattgccc     600
ccgctctgga tctggtctag cttccggatt cggtggccag tccgcggggt gtagatgttc     660
ctgacggccc caaagggtgc ctgaacgccg ccggtcacct ccttcaggaa gacttcgaag     720
ctggacacct tcttctc atg gat gac gac gcg gcg ccc cgc gta gaa ggg        770
                    Met Asp Asp Asp Ala Ala Pro Arg Val Glu Gly
                     1               5                   10
gtc ccc gtt gcg gta cac aag cac gct ctt cac gac ggg ctg aga cag     818
Val Pro Val Ala Val His Lys His Ala Leu His Asp Gly Leu Arg Gln
            15                  20                  25
gtg gct gga cct ggc gct gct gcc gct cat ctt ccc cgc tgg ccg ccg     866
Val Ala Gly Pro Gly Ala Ala Ala Ala His Leu Pro Arg Trp Pro Pro
            30                  35                  40
cct cag ctc gct gct tcg cgt cgg gag gca cct ccg ctg tcc cag cgg     914
Pro Gln Leu Ala Ala Ser Arg Arg Glu Ala Pro Pro Leu Ser Gln Arg
        45                  50                  55
cct cac cgc acc cag ggc gcg gga tcg cct cct gaa acg aac gag aaa     962
Pro His Arg Thr Gln Gly Ala Gly Ser Pro Pro Glu Thr Asn Glu Lys
60                  65                  70                  75
ctg acg aat cca cag gtg aaa gag aag taacggccgt gcgcctaggc gtccacc    1016
Leu Thr Asn Pro Gln Val Lys Glu Lys
                80
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cagaggagac actaggagct tgcaggactc ggagtagacg ctcaagtttt tcaccgtggc    1076
gtgcacagcc aatcaggacc cgcagtgcgc gcaccacacc aggttcacct gctacgggca    1136
gaatcaaggt ggacagcttc tgagcaggag ccggaaacgc gcggggcctt caaacaggca    1196
cgcctagtga gggcaggaga gaggaggacg cacacacaca cacacacaca aatatggtga    1256
aacccaattt cttacatcat atctgtgcta ccctttccaa acagcctaat ttttcttttc    1316
tctcttcttg cacctttacc cctcaatctc ctgcttcctc ccaaattaaa gcaattaagt    1376
tcctgg                                                                1382
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        <212> PRT
        <213> Homo sapiens


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His Lys His Ala Leu His Asp Gly Leu Arg Gln Val Ala Gly Pro Gly
                20                  25                  30
Ala Ala Ala Ala His Leu Pro Arg Trp Pro Pro Pro Gln Leu Ala Ala
        35                  40                  45
Ser Arg Arg Glu Ala Pro Pro Leu Ser Gln Arg Pro His Arg Thr Gln
    50                  55                  60
Gly Ala Gly Ser Pro Pro Glu Thr Asn Glu Lys Leu Thr Asn Pro Gln
65                  70                  75                  80
Val Lys Glu Lys


        <210> 3
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        <213> Homo sapiens


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Leu Pro Arg Trp Pro Pro Pro Gln Leu
1               5


        <210> 4
        <211> 2167
        <212> DNA
        <213> Homo sapiens


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        <222> 303..1730


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tagtgtctcc tctgggtgga cgcctaggcg cacggccgtt acttctcttt cacctgtgga      180
ttcgtcagtt tctcgttcgt ttcaggaggc gatcccgcgc cctgggtgcg gtgaggccgc      240
tgggacagcg gaggtgcctc ccgacgcgaa gcagcgagct gaggcggcgg ccagcgggga      300
ag atg agc ggc agc agc gcc agg tcc agc cac ctg tct cag ccc gtc         347
   Met Ser Gly Ser Ser Ala Arg Ser Ser His Leu Ser Gln Pro Val
   1               5                   10                  15
gtg aag agc gtg ctt gtg tac cgc aac ggg gac ccc ttc tac gcg ggg        395
Val Lys Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly
                20                  25                  30
cgc cgc gtc gtc atc cat gag aag aag gtg tcc agc ttc gaa gtc ttc        443
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                Arg Arg Val Val Ile His Glu Lys Lys Val Ser Ser Phe Glu Val Phe
                            35                  40                  45
ctg aag gag gtg acc ggc ggc gtt cag gca ccc ttt ggg gcc gtc agg        491
Leu Lys Glu Val Thr Gly Gly Val Gln Ala Pro Phe Gly Ala Val Arg
        50                  55                  60
aac atc tac acc ccg cgg act ggc cac cga atc cgg aag cta gac cag        539
Asn Ile Tyr Thr Pro Arg Thr Gly His Arg Ile Arg Lys Leu Asp Gln
        65                  70                  75
atc cag agc ggg ggc aat tac gtg gct gga ggc cag gaa gcc ttc aag        587
Ile Gln Ser Gly Gly Asn Tyr Val Ala Gly Gly Gln Glu Ala Phe Lys
80                  85                  90                  95
aaa ctc aat tac ttg gac ata gga gaa atc aag aaa aga cca atg gaa        635
Lys Leu Asn Tyr Leu Asp Ile Gly Glu Ile Lys Lys Arg Pro Met Glu
                    100                 105                 110
gtt gtt aat aca gag gta aaa cca gta atc cat agc agg atc aac gtg        683
Val Val Asn Thr Glu Val Lys Pro Val Ile His Ser Arg Ile Asn Val
            115                 120                 125
tca gct cgc ttt aga aaa ccg ctt cag gag ccg tgc act atc ttc ttg       731
Ser Ala Arg Phe Arg Lys Pro Leu Gln Glu Pro Cys Thr Ile Phe Leu
            130                 135                 140
att gca aat gga gac ctc ata aac cca gct tct cgc ctc ctt atc ccc       779
Ile Ala Asn Gly Asp Leu Ile Asn Pro Ala Ser Arg Leu Leu Ile Pro
            145                 150                 155
aga aaa acc ttg aat cag tgg gat cat gta cta caa atg gtc aca gaa       827
Arg Lys Thr Leu Asn Gln Trp Asp His Val Leu Gln Met Val Thr Glu
160                 165                 170                 175
aaa atc act ctg agg agc ggg gct gtt cac agg ctt tat act tta gaa       875
Lys Ile Thr Leu Arg Ser Gly Ala Val His Arg Leu Tyr Thr Leu Glu
                    180                 185                 190
gga aaa ctt gtt gag agt gga gca gag ttg gag aat ggg cag ttt tat       923
Gly Lys Leu Val Glu Ser Gly Ala Glu Leu Glu Asn Gly Gln Phe Tyr
            195                 200                 205
gtg gct gtt ggc aga gat aag ttt aag aaa ctg cct tac ggt gag tta       971
Val Ala Val Gly Arg Asp Lys Phe Lys Lys Leu Pro Tyr Gly Glu Leu
            210                 215                 220
ctt ttt gac aag tca acg atg aga agg cct ttt ggt cag aaa gct tct      1019
Leu Phe Asp Lys Ser Thr Met Arg Arg Pro Phe Gly Gln Lys Ala Ser
            225                 230                 235
tca cta cct cct att gta gga tcc aga aag tct aaa ggg agt gga aat      1067
Ser Leu Pro Pro Ile Val Gly Ser Arg Lys Ser Lys Gly Ser Gly Asn
240                 245                 250                 255
gat cgc cac tct aag tca aca gtt gga tcc agt gac aac tca tct cct      1115
Asp Arg His Ser Lys Ser Thr Val Gly Ser Ser Asp Asn Ser Ser Pro
                    260                 265                 270
cag ccc ctg aag agg aaa ggg aaa aaa gaa gac gtg aat tca gaa aaa      1163
Gln Pro Leu Lys Arg Lys Gly Lys Lys Glu Asp Val Asn Ser Glu Lys
            275                 280                 285
ctg acg aaa ttg aaa caa aat gta aaa tta aag aat tca caa gaa acc      1211
Leu Thr Lys Leu Lys Gln Asn Val Lys Leu Lys Asn Ser Gln Glu Thr
            290                 295                 300
att cca aat agt gat gaa ggc att ttc aaa gct gga gca gag agg tct      1259
Ile Pro Asn Ser Asp Glu Gly Ile Phe Lys Ala Gly Ala Glu Arg Ser
            305                 310                 315
gaa aca cgg ggg gca gca gaa gtc caa gaa gat gaa gat act cag gtt      1307
Glu Thr Arg Gly Ala Ala Glu Val Gln Glu Asp Glu Asp Thr Gln Val
320                 325                 330                 335
gag gtt cca gtc gat cag agg cca gca gaa ata gta gac gag gaa gaa      1355
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- 4 -

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Glu Val Pro Val Asp Gln Arg Pro Ala Glu Ile Val Asp Glu Glu Glu
                340                 345                 350
gat gga gag aag gca aac aag gat gca gaa cag aaa gaa gac ttt tca    1403
Asp Gly Glu Lys Ala Asn Lys Asp Ala Glu Gln Lys Glu Asp Phe Ser
                355                 360                 365
gga atg aat ggt gac ctt gaa gag gaa gga ggt agg gag gct aca gat    1451
Gly Met Asn Gly Asp Leu Glu Glu Glu Gly Gly Arg Glu Ala Thr Asp
                370                 375                 380
gcc cct gag caa gtc gag gag att ctg gat cac agt gag cag cag gca    1499
Ala Pro Glu Gln Val Glu Glu Ile Leu Asp His Ser Glu Gln Gln Ala
                385                 390                 395
cgc cct gct cgt gta aat gga ggc acc gat gag gag aat ggt gag gag    1547
Arg Pro Ala Arg Val Asn Gly Gly Thr Asp Glu Glu Asn Gly Glu Glu
400                 405                 410                 415
ctg cag cag gtt aat aat gag ctt caa ctg gtc cta gac aag gaa aga    1595
Leu Gln Gln Val Asn Asn Glu Leu Gln Leu Val Leu Asp Lys Glu Arg
                420                 425                 430
aag tct caa gga gct ggc agt gga caa gat gag gct gat gta gac cct    1643
Lys Ser Gln Gly Ala Gly Ser Gly Gln Asp Glu Ala Asp Val Asp Pro
                435                 440                 445
caa aga cca cca agg cca gaa gta aaa att acc agt cca gaa gaa aat    1691
Gln Arg Pro Pro Arg Pro Glu Val Lys Ile Thr Ser Pro Glu Glu Asn
                450                 455                 460
gaa aac aac caa caa aac aag gac tat gct gcc gtg gct tagaagattt tt    1742
Glu Asn Asn Gln Gln Asn Lys Asp Tyr Ala Ala Val Ala
465                 470                 475
aaaaagagag tatatggatc gcaagaaaaa tgaagggtta tcatacttga aagataagca    1802
catagttatt gctgaatata atgtgacact atggtcgaat actacctacg aattataaca    1862
ttagaagcct agtggaaaga ccagataact ttaaatggct actaaaggat aattacttac    1922
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tttgcactgg aagacaattg ccacttgtaa aggatgaaaa ataggatcac tcttattgta    2042
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        <213>  Homo sapiens

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Lys Ser Val Leu Val Tyr Arg Asn Gly Asp Pro Phe Tyr Ala Gly Arg
                20                  25                  30
Arg Val Val Ile His Glu Lys Lys Val Ser Ser Phe Glu Val Phe Leu
                35                  40                  45
Lys Glu Val Thr Gly Gly Val Gln Ala Pro Phe Gly Ala Val Arg Asn
                50                  55                  60
Ile Tyr Thr Pro Arg Thr Gly His Arg Ile Arg Lys Leu Asp Gln Ile
65                  70                  75                  80
Gln Ser Gly Gly Asn Tyr Val Ala Gly Gly Gln Glu Ala Phe Lys Lys
                85                  90                  95
Leu Asn Tyr Leu Asp Ile Gly Glu Ile Lys Lys Arg Pro Met Glu Val
                100                 105                 110
Val Asn Thr Glu Val Lys Pro Val Ile His Ser Arg Ile Asn Val Ser
                115                 120                 125
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Ala Arg Phe Arg Lys Pro Leu Gln Glu Pro Cys Thr Ile Phe Leu Ile
    130                 135                 140
Ala Asn Gly Asp Leu Ile Asn Pro Ala Ser Arg Leu Leu Ile Pro Arg
145                 150                 155                 160
Lys Thr Leu Asn Gln Trp Asp His Val Leu Gln Met Val Thr Glu Lys
                165                 170                 175
Ile Thr Leu Arg Ser Gly Ala Val His Arg Leu Tyr Thr Leu Glu Gly
                180                 185                 190
Lys Leu Val Glu Ser Gly Ala Glu Leu Glu Asn Gly Gln Phe Tyr Val
                195                 200                 205
Ala Val Gly Arg Asp Lys Phe Lys Lys Leu Pro Tyr Gly Glu Leu Leu
    210                 215                 220
Phe Asp Lys Ser Thr Met Arg Arg Pro Phe Gly Gln Lys Ala Ser Ser
225                 230                 235                 240
Leu Pro Pro Ile Val Gly Ser Arg Lys Ser Lys Gly Ser Gly Asn Asp
                245                 250                 255
Arg His Ser Lys Ser Thr Val Gly Ser Ser Asp Asn Ser Ser Pro Gln
                260                 265                 270
Pro Leu Lys Arg Lys Gly Lys Lys Glu Asp Val Asn Ser Glu Lys Leu
                275                 280                 285
Thr Lys Leu Lys Gln Asn Val Lys Leu Lys Asn Ser Gln Glu Thr Ile
    290                 295                 300
Pro Asn Ser Asp Glu Gly Ile Phe Lys Ala Gly Ala Glu Arg Ser Glu
305                 310                 315                 320
Thr Arg Gly Ala Ala Glu Val Gln Glu Asp Glu Asp Thr Gln Val Glu
                325                 330                 335
Val Pro Val Asp Gln Arg Pro Ala Glu Ile Val Asp Glu Glu Glu Asp
                340                 345                 350
Gly Glu Lys Ala Asn Lys Asp Ala Glu Gln Lys Glu Asp Phe Ser Gly
    355                 360                 365
Met Asn Gly Asp Leu Glu Glu Glu Gly Gly Arg Glu Ala Thr Asp Ala
    370                 375                 380
Pro Glu Gln Val Glu Glu Ile Leu Asp His Ser Glu Gln Gln Ala Arg
385                 390                 395                 400
Pro Ala Arg Val Asn Gly Gly Thr Asp Glu Glu Asn Gly Glu Glu Leu
                405                 410                 415
Gln Gln Val Asn Asn Glu Leu Gln Leu Val Leu Asp Lys Glu Arg Lys
                420                 425                 430
Ser Gln Gly Ala Gly Ser Gly Gln Asp Glu Ala Asp Val Asp Pro Gln
    435                 440                 445
Arg Pro Pro Arg Pro Glu Val Lys Ile Thr Ser Pro Glu Glu Asn Glu
    450                 455                 460
Asn Asn Gln Gln Asn Lys Asp Tyr Ala Ala Val Ala
465                 470                 475
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<212> DNA
<213> Homo sapiens

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<211> 18
<212> DNA
<213> Homo sapiens
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    <210> 8
    <211> 25
    <212> DNA
    <213> Homo sapiens

    <400> 8
taaatgggtg ggcggtgggg gagac                                           25

    <210> 9
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    <212> DNA
    <213> Homo sapiens

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taggctgttt ggaaagggta gcaca                                           25

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    <212> DNA
    <213> Homo sapiens

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agattttaag tttactccta ctgctgaccc aagtgaaatt ccttctccag tcacagtgtc   120
aacctctacc ccccaactgc aacgagagtt ttgaggggca tcaatcacac cgagaagtca   180
cagcccctca accactgagg tgtggggggg tagggatctg catttcttca tatcaacccc   240
acacta                                                              246

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    <221> unsure
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<223> n = a, c, g or t

<220>
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<222> 591..591
<223> n = a, c, g or t

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ggcgtagaat tttaaagaac tggtaatagg aaagcatgta ctattttctt aaagcaataa    180
actcttgaat gaacagattg cgatttactt tcagacataa tttggagatg gcagtagatc    240
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cctttttgact acaaatnccn gagcaaggcg ttcattttttg gtgggaagga agcattgggt    360
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ccngttanag tttataaagc ctggatggta tggttngccg agtaatgnga aatcctgtgg    540
gantttccac tgatccaggt ccaatcttta cccagtagnt atctctctcc ntctcccotta    600
tgttattggg gaa    613
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